

SEQUENCE LISTING

<110> Commissariat à l'Etude Atomique (CEA)
Centre National de la Recherche Scientifique (CNRS)

<120> A method for performing restrained dynamics docking of one or multiple substrates on multi-specific enzymes

<130> D20647

<150> US 60/421,569

<151> 2002-10-28

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 403

<212> PRT

<213> Fusarium oxysporum

<220>

<223> P450 Nor, crystal structure from

<400> 1

Met Ala Ser Gly Ala Pro Ser Phe Pro Phe Ser Arg Ala Ser Gly Pro
1 5 10 15

Glu Pro Pro Ala Glu Phe Ala Lys Leu Arg Ala Thr Asn Pro Val Ser
20 25 30

Gln Val Lys Leu Phe Asp Gly Ser Leu Ala Trp Leu Val Thr Lys His
35 40 45

Lys Asp Val Cys Phe Val Ala Thr Ser Glu Lys Leu Ser Lys Val Arg
50 55 60

Thr Arg Gln Gly Phe Pro Glu Leu Ser Ala Ser Gly Lys Gln Ala Ala
65 70 75 80

Lys Ala Lys Pro Thr Phe Val Asp Met Asp Pro Pro Glu His Met His
85 90 95

Gln Arg Ser Met Val Glu Pro Thr Phe Thr Pro Glu Ala Val Lys Asn
100 105 110

Leu Gln Pro Tyr Ile Gln Arg Thr Val Asp Asp Leu Leu Glu Gln Met
115 120 125

Lys Gln Lys Gly Cys Ala Asn Gly Pro Val Asp Leu Val Lys Glu Phe
130 135 140

Ala Leu Pro Val Pro Ser Tyr Ile Ile Tyr Thr Leu Leu Gly Val Pro
145 150 155 160

Phe Asn Asp Leu Glu Tyr Leu Thr Gln Gln Asn Ala Ile Arg Thr Asn
165 170 175

Gly Ser Ser Thr Ala Arg Glu Ala Ser Ala Ala Asn Gln Glu Leu Leu
 180 185 190
 Asp Tyr Leu Ala Ile Leu Val Glu Gln Arg Leu Val Glu Pro Lys Asp
 195 200 205
 Asp Ile Ile Ser Lys Leu Cys Thr Glu Gln Val Lys Pro Gly Asn Ile
 210 215 220
 Asp Lys Ser Asp Ala Val Gln Ile Ala Phe Leu Leu Leu Val Ala Gly
 225 230 235 240
 Asn Ala Thr Met Val Asn Met Ile Ala Leu Gly Val Ala Thr Leu Ala
 245 250 255
 Gln His Pro Asp Gln Leu Ala Gln Leu Lys Ala Asn Pro Ser Leu Ala
 260 265 270
 Pro Gln Phe Val Glu Glu Leu Cys Arg Tyr His Thr Ala Ser Ala Leu
 275 280 285
 Ala Ile Lys Arg Thr Ala Lys Glu Asp Val Met Ile Gly Asp Lys Leu
 290 295 300
 Val Arg Ala Asn Glu Gly Ile Ile Ala Ser Asn Gln Ser Ala Asn Arg
 305 310 315 320
 Asp Glu Glu Val Phe Glu Asn Pro Asp Glu Phe Asn Met Asn Arg Lys
 325 330 335
 Trp Pro Pro Gln Asp Pro Leu Gly Phe Gly Phe Gly Asp His Arg Cys
 340 345 350
 Ile Ala Glu His Leu Ala Lys Ala Glu Leu Thr Thr Val Phe Ser Thr
 355 360 365
 Leu Tyr Gln Lys Phe Pro Asp Leu Lys Val Ala Val Pro Leu Gly Lys
 370 375 380
 Ile Asn Tyr Thr Pro Leu Asn Arg Asp Val Gly Ile Val Asp Leu Pro
 385 390 395 400
 Val Ile Phe

<210> 2

<211> 403

<212> PRT

<213> Saccharopolyspora erythraea

<220>

<223> P450 EryF, crystal structure loxa

<400> 2

Ala Thr Val Pro Asp Leu Glu Ser Asp Ser Phe His Val Asp Trp Tyr
 1 5 10 15

Ser Thr Tyr Ala Glu Leu Arg Glu Thr Ala Pro Val Thr Pro Val Arg
 20 25 30

Phe Leu Gly Gln Asp Ala Trp Leu Val Thr Gly Tyr Asp Glu Ala Lys
 35 40 45
 Ala Ala Leu Ser Asp Leu Arg Leu Ser Ser Asp Pro Lys Lys Lys Tyr
 50 55 60
 Pro Gly Val Glu Val Glu Phe Pro Ala Tyr Leu Gly Phe Pro Glu Asp
 65 70 75 80
 Val Arg Asn Tyr Phe Ala Thr Asn Met Gly Thr Ser Asp Pro Pro Thr
 85 90 95
 His Thr Arg Leu Arg Lys Leu Val Ser Gln Glu Phe Thr Val Arg Arg
 100 105 110
 Val Glu Ala Met Arg Pro Arg Val Glu Gln Ile Thr Ala Glu Leu Leu
 115 120 125
 Asp Glu Val Gly Asp Ser Gly Val Val Asp Ile Val Asp Arg Phe Ala
 130 135 140
 His Pro Leu Pro Ile Lys Val Ile Cys Glu Leu Leu Gly Val Asp Glu
 145 150 155 160
 Ala Ala Arg Gly Ala Phe Gly Arg Trp Ser Ser Glu Ile Leu Val Met
 165 170 175
 Asp Pro Glu Arg Ala Glu Gln Arg Gly Gln Ala Ala Arg Glu Val Val
 180 185 190
 Asn Phe Ile Leu Asp Leu Val Glu Arg Arg Arg Thr Glu Pro Gly Asp
 195 200 205
 Asp Leu Leu Ser Ala Leu Ile Ser Val Gln Asp Asp Asp Asp Gly Arg
 210 215 220
 Leu Ser Ala Asp Glu Leu Thr Ser Ile Ala Leu Val Leu Leu Leu Ala
 225 230 235 240
 Gly Phe Glu Ala Ser Val Ser Leu Ile Gly Ile Gly Thr Tyr Leu Leu
 245 250 255
 Leu Thr His Pro Asp Gln Leu Ala Leu Val Arg Ala Asp Pro Ser Ala
 260 265 270
 Leu Pro Asn Ala Val Glu Glu Ile Leu Arg Tyr Ile Ala Pro Pro Glu
 275 280 285
 Thr Thr Thr Arg Phe Ala Ala Glu Glu Val Glu Ile Gly Gly Val Ala
 290 295 300
 Ile Pro Gln Tyr Ser Thr Val Leu Val Ala Asn Gly Ala Ala Asn Arg
 305 310 315 320
 Asp Pro Ser Gln Phe Pro Asp Pro His Arg Phe Asp Val Thr Arg Asp
 325 330 335
 Thr Arg Gly His Leu Ser Phe Gly Gln Gly Ile His Phe Cys Met Gly
 340 345 350
 Arg Pro Leu Ala Lys Leu Glu Gly Glu Val Ala Leu Arg Ala Leu Phe

355 360 365
 Gly Arg Phe Pro Ala Leu Ser Leu Gly Ile Asp Ala Asp Asp Val Val
 370 375 380
 Trp Arg Arg Ser Leu Leu Leu Arg Gly Ile Asp His Leu Pro Val Arg
 385 390 395 400
 Leu Asp Gly

 <210> 3
 <211> 412
 <212> PRT
 <213> Pseudomonas sp.

 <220>
 <223> P450 Terp, crystal structure 1cpt

 <400> 3
 Met Asp Ala Arg Ala Thr Ile Pro Glu His Ile Ala Arg Thr Val Ile
 1 5 10 15
 Leu Pro Gln Gly Tyr Ala Asp Asp Glu Val Ile Tyr Pro Ala Phe Lys
 20 25 30
 Trp Leu Arg Asp Glu Gln Pro Leu Ala Met Ala His Ile Glu Gly Tyr
 35 40 45
 Asp Pro Met Trp Ile Ala Thr Lys His Ala Asp Val Met Gln Ile Gly
 50 55 60
 Lys Gln Pro Gly Leu Phe Ser Asn Ala Glu Gly Ser Glu Ile Leu Tyr
 65 70 75 80
 Asp Gln Asn Asn Glu Ala Phe Met Arg Ser Ile Ser Gly Gly Cys Pro
 85 90 95
 His Val Ile Asp Ser Leu Thr Ser Met Asp Pro Pro Thr His Thr Ala
 100 105 110
 Tyr Arg Gly Leu Thr Leu Asn Trp Phe Gln Pro Ala Ser Ile Arg Lys
 115 120 125
 Leu Glu Glu Asn Ile Arg Arg Ile Ala Gln Ala Ser Val Gln Arg Leu
 130 135 140
 Leu Asp Phe Asp Gly Glu Cys Asp Phe Met Thr Asp Cys Ala Leu Tyr
 145 150 155 160
 Tyr Pro Leu His Val Val Met Thr Ala Leu Gly Val Pro Glu Asp Asp
 165 170 175
 Glu Pro Leu Met Leu Lys Leu Thr Gln Asp Phe Phe Gly Val Glu Ala
 180 185 190
 Ala Arg Arg Phe His Glu Thr Ile Ala Thr Phe Tyr Asp Tyr Phe Asn
 195 200 205
 Gly Phe Thr Val Asp Arg Arg Ser Cys Pro Lys Asp Asp Val Met Ser

210 215 220
 Leu Leu Ala Asn Ser Lys Leu Asp Gly Asn Tyr Ile Asp Asp Lys Tyr
 225 230 235 240
 Ile Asn Ala Tyr Tyr Val Ala Ile Ala Thr Ala Gly His Asp Thr Thr
 245 250 255
 Ser Ser Ser Ser Gly Gly Ala Ile Ile Gly Leu Ser Arg Asn Pro Glu
 260 265 270
 Gln Leu Ala Leu Ala Lys Ser Asp Pro Ala Leu Ile Pro Arg Leu Val
 275 280 285
 Asp Glu Ala Val Arg Trp Thr Ala Pro Val Lys Ser Phe Met Arg Thr
 290 295 300
 Ala Leu Ala Asp Thr Glu Val Arg Gly Gln Asn Ile Lys Arg Gly Asp
 305 310 315 320
 Arg Ile Met Leu Ser Tyr Pro Ser Ala Asn Arg Asp Glu Glu Val Phe
 325 330 335
 Ser Asn Pro Asp Glu Phe Asp Ile Thr Arg Phe Pro Asn Arg His Leu
 340 345 350
 Gly Phe Gly Trp Gly Ala His Met Cys Leu Gly Gln His Leu Ala Lys
 355 360 365
 Leu Glu Met Lys Ile Phe Phe Glu Glu Leu Leu Pro Lys Leu Lys Ser
 370 375 380
 Val Glu Leu Ser Gly Pro Pro Arg Leu Val Ala Thr Asn Phe Val Gly
 385 390 395 400
 Gly Pro Lys Asn Val Pro Ile Arg Phe Thr Lys Ala
 405 410

<210> 4

<211> 414

<212> PRT

<213> Pseudomonas putida

<220>

<223> P450 Cam, crystal structure 3cpp

<400> 4

Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro
 1 5 10 15
 His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser
 20 25 30
 Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser
 35 40 45
 Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile
 50 55 60
 Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His

65				70				75				80			
Phe	Ser	Ser	Glu	Cys 85	Pro	Phe	Ile	Pro	Arg	Glu	Ala	Gly	Glu	Ala	Tyr
Asp	Phe	Ile	Pro 100	Thr	Ser	Met	Asp	Pro 105	Pro	Glu	Gln	Arg	Gln 110	Phe	Arg
Ala	Leu	Ala 115	Asn	Gln	Val	Val	Gly 120	Met	Pro	Val	Val	Asp 125	Lys	Leu	Glu
Asn	Arg 130	Ile	Gln	Glu	Leu	Ala 135	Cys	Ser	Leu	Ile	Glu 140	Ser	Leu	Arg	Pro
Gln 145	Gly	Gln	Cys	Asn 150	Phe	Thr	Glu	Asp	Tyr	Ala 155	Glu	Pro	Phe	Pro	Ile 160
Arg	Ile	Phe	Met	Leu 165	Leu	Ala	Gly	Leu	Pro 170	Glu	Glu	Asp	Ile	Pro	His
Leu	Lys	Tyr	Leu 180	Thr	Asp	Gln	Met	Thr 185	Arg	Pro	Asp	Gly	Ser 190	Met	Thr
Phe	Ala	Glu 195	Ala	Lys	Glu	Ala	Leu 200	Tyr	Asp	Tyr	Leu	Ile 205	Pro	Ile	Ile
Glu	Gln 210	Arg	Arg	Gln	Lys	Pro 215	Gly	Thr	Asp	Ala	Ile 220	Ser	Ile	Val	Ala
Asn 225	Gly	Gln	Val	Asn 230	Gly	Arg	Pro	Ile	Thr	Ser 235	Asp	Glu	Ala	Lys	Arg 240
Met	Cys	Gly	Leu	Leu 245	Leu	Val	Gly	Gly	Leu 250	Asp	Thr	Val	Val	Asn 255	Phe
Leu	Ser	Phe	Ser 260	Met	Glu	Phe	Leu	Ala 265	Lys	Ser	Pro	Glu	His 270	Arg	Gln
Glu	Leu	Ile 275	Glu	Arg	Pro	Glu	Arg 280	Ile	Pro	Ala	Ala	Cys 285	Glu	Glu	Leu
Leu	Arg 290	Arg	Phe	Ser	Leu	Val 295	Ala	Asp	Gly	Arg	Ile 300	Leu	Thr	Ser	Asp
Tyr 305	Glu	Phe	His	Gly 310	Val	Gln	Leu	Lys	Lys	Gly 315	Asp	Gln	Ile	Leu	Leu 320
Pro	Gln	Met	Leu	Ser 325	Gly	Leu	Asp	Glu	Arg 330	Glu	Asn	Ala	Cys	Pro 335	Met
His	Val	Asp	Phe 340	Ser	Arg	Gln	Lys	Val 345	Ser	His	Thr	Thr	Phe 350	Gly	His
Gly	Ser	His 355	Leu	Cys	Leu	Gly	Gln 360	His	Leu	Ala	Arg	Arg 365	Glu	Ile	Ile
Val	Thr 370	Leu	Lys	Glu	Trp	Leu 375	Thr	Arg	Ile	Pro	Asp 380	Phe	Ser	Ile	Ala
Pro 385	Gly	Ala	Gln	Ile 390	Gln	His	Lys	Ser	Gly	Ile 395	Val	Ser	Gly	Val	Gln 400

Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
 405 410

<210> 5

<211> 471

<212> PRT

<213> Bacillus megaterium

<220>

<223> P450 BM3, crystal structure 2hpd

<400> 5

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn
 1 5 10 15

Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
 20 25 30

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
 35 40 45

Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
 50 55 60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
 65 70 75 80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp
 85 90 95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
 100 105 110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
 115 120 125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
 130 135 140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
 145 150 155 160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
 165 170 175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
 180 185 190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
 195 200 205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
 210 215 220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
 225 230 235 240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr

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245	250	255
Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu		
260	265	270
Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln		
275	280	285
Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser		
290	295	300
Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu		
305	310	315
Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys		
325	330	335
Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu		
340	345	350
Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly		
355	360	365
Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala		
370	375	380
Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys		
385	390	395
Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met		
405	410	415
Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp		
420	425	430
Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala		
435	440	445
Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu		
450	455	460
Gln Ser Ala Lys Lys Val Arg		
465	470	

<210> 6

<211> 473

<212> PRT

<213> Rabbit

<220>

<223> P450 2C5, crystal structure 1dt6

<400> 6

Met	Ala	Lys	Lys	Thr	Ser	Ser	Lys	Gly	Lys	Leu	Pro	Pro	Gly	Pro	Thr
1				5				10					15		

Pro	Phe	Pro	Ile	Ile	Gly	Asn	Ile	Leu	Gln	Ile	Asp	Ala	Lys	Asp	Ile
			20					25					30		

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Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val Phe Thr
 35 40 45
 Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr Glu Ala
 50 55 60
 Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly Arg Gly
 65 70 75 80
 Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile Ala Phe
 85 90 95
 Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu Met Thr
 100 105 110
 Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Ile Gln
 115 120 125
 Glu Glu Ala Arg Cys Leu Val Glu Glu Leu Arg Lys Thr Asn Ala Ser
 130 135 140
 Pro Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn Val Ile
 145 150 155 160
 Cys Ser Val Ile Phe His Asn Arg Phe Asp Tyr Lys Asp Glu Glu Phe
 165 170 175
 Leu Lys Leu Met Glu Ser Leu His Glu Asn Val Glu Leu Leu Gly Thr
 180 185 190
 Pro Trp Leu Gln Val Tyr Asn Asn Phe Pro Ala Leu Leu Asp Tyr Phe
 195 200 205
 Pro Gly Ile His Lys Thr Leu Leu Lys Asn Ala Asp Tyr Ile Lys Asn
 210 215 220
 Phe Ile Met Glu Lys Val Lys Glu His Gln Lys Leu Leu Asp Val Asn
 225 230 235 240
 Asn Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu Gln Glu
 245 250 255
 Asn Asn Leu Glu Phe Thr Leu Glu Ser Leu Val Ile Ala Val Ser Asp
 260 265 270
 Leu Phe Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg Tyr Ser
 275 280 285
 Leu Leu Leu Leu Leu Lys His Pro Glu Val Ala Ala Arg Val Gln Glu
 290 295 300
 Glu Ile Glu Arg Val Ile Gly Arg His Arg Ser Pro Cys Met Gln Asp
 305 310 315 320
 Arg Ser Arg Met Pro Tyr Thr Asp Ala Val Ile His Glu Ile Gln Arg
 325 330 335
 Phe Ile Asp Leu Leu Pro Thr Asn Leu Pro His Ala Val Thr Arg Asp
 340 345 350
 Val Arg Phe Arg Asn Tyr Phe Ile Pro Lys Gly Thr Asp Ile Ile Thr

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355	360	365
Ser Leu Thr Ser Val Leu His Asp Glu Lys Ala Phe Pro Asn Pro Lys		
370	375	380
Val Phe Asp Pro Gly His Phe Leu Asp Glu Ser Gly Asn Phe Lys Lys		
385	390	395 400
Ser Asp Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Met Cys Val Gly		
405	410	415
Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Ser Ile Leu		
420	425	430
Gln Asn Phe Lys Leu Gln Ser Leu Val Glu Pro Lys Asp Leu Asp Ile		
435	440	445
Thr Ala Val Val Asn Gly Phe Val Ser Val Pro Pro Ser Tyr Gln Leu		
450	455	460
Cys Phe Ile Pro Ile His His His His		
465	470	

<210> 7
 <211> 487
 <212> PRT
 <213> Rabbit

<220>
 <223> P450 2C5

<400> 7

Met Asp Pro Val Val Val Leu Val Leu Gly Leu Cys Cys Leu Leu Leu	
1 5 10 15	
Leu Ser Ile Trp Lys Gln Asn Ser Gly Arg Gly Lys Leu Pro Pro Gly	
20 25 30	
Pro Thr Pro Phe Pro Ile Ile Gly Asn Ile Leu Gln Ile Asp Ala Lys	
35 40 45	
Asp Ile Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val	
50 55 60	
Phe Thr Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr	
65 70 75 80	
Glu Ala Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly	
85 90 95	
Thr Gly Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile	
100 105 110	
Ala Phe Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu	
115 120 125	
Met Thr Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg	
130 135 140	

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Ile	Gln	Glu	Glu	Ala	Arg	Cys	Leu	Val	Glu	Glu	Leu	Arg	Lys	Thr	Asn	145	150	155	160
Ala	Ser	Pro	Cys	Asp	Pro	Thr	Phe	Ile	Leu	Gly	Cys	Ala	Pro	Cys	Asn	165	170	175	
Val	Ile	Cys	Ser	Val	Ile	Phe	His	Asn	Arg	Phe	Asp	Tyr	Lys	Asp	Glu	180	185	190	
Glu	Phe	Leu	Lys	Leu	Met	Glu	Ser	Leu	Asn	Glu	Asn	Val	Arg	Ile	Leu	195	200	205	
Ser	Ser	Pro	Trp	Leu	Gln	Val	Tyr	Asn	Asn	Phe	Pro	Ala	Leu	Leu	Asp	210	215	220	
Tyr	Phe	Pro	Gly	Ile	His	Lys	Thr	Leu	Leu	Lys	Asn	Ala	Asp	Tyr	Ile	225	230	235	240
Lys	Asn	Phe	Ile	Met	Glu	Lys	Val	Lys	Glu	His	Glu	Lys	Leu	Leu	Asp	245	250	255	
Val	Asn	Asn	Pro	Arg	Asp	Phe	Ile	Asp	Cys	Phe	Leu	Ile	Lys	Met	Glu	260	265	270	
Gln	Glu	Asn	Asn	Leu	Glu	Phe	Thr	Leu	Glu	Ser	Leu	Val	Ile	Ala	Val	275	280	285	
Ser	Asp	Leu	Phe	Gly	Ala	Gly	Thr	Glu	Thr	Thr	Ser	Thr	Thr	Leu	Arg	290	295	300	
Tyr	Ser	Leu	Leu	Leu	Leu	Leu	Lys	His	Pro	Glu	Val	Ala	Ala	Arg	Val	305	310	315	320
Gln	Glu	Glu	Ile	Glu	Arg	Val	Ile	Gly	Arg	His	Arg	Ser	Pro	Cys	Met	325	330	335	
Gln	Asp	Arg	Ser	Arg	Met	Pro	Tyr	Thr	Asp	Ala	Val	Ile	His	Glu	Ile	340	345	350	
Gln	Arg	Phe	Ile	Asp	Leu	Leu	Pro	Thr	Asn	Leu	Pro	His	Ala	Val	Thr	355	360	365	
Arg	Asp	Val	Arg	Phe	Arg	Asn	Tyr	Phe	Ile	Pro	Lys	Gly	Thr	Asp	Ile	370	375	380	
Ile	Thr	Ser	Leu	Thr	Ser	Val	Leu	His	Asp	Glu	Lys	Ala	Phe	Pro	Asn	385	390	395	400
Pro	Lys	Val	Phe	Asp	Pro	Gly	His	Phe	Leu	Asp	Glu	Ser	Gly	Asn	Phe	405	410	415	
Lys	Lys	Ser	Asp	Tyr	Phe	Met	Pro	Phe	Ser	Ala	Gly	Lys	Arg	Met	Cys	420	425	430	
Val	Gly	Glu	Gly	Leu	Ala	Arg	Met	Glu	Leu	Phe	Leu	Phe	Leu	Thr	Ser	435	440	445	
Ile	Leu	Gln	Asn	Phe	Lys	Leu	Gln	Ser	Leu	Val	Glu	Pro	Lys	Asp	Leu	450	455	460	
Asp	Ile	Thr	Ala	Val	Val	Asn	Gly	Phe	Val	Ser	Val	Pro	Pro	Ser	Tyr				

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465

470

475

480

Gln Leu Cys Phe Ile Pro Ile
485

<210> 8

<211> 455

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> CYP51, crystal structure 1e9x

<400> 8

Met Ser Ala Val Ala Leu Pro Arg Val Ser Gly Gly His Asp Glu His
1 5 10 15

Gly His Leu Glu Glu Phe Arg Thr Asp Pro Ile Gly Leu Met Gln Arg
20 25 30

Val Arg Asp Glu Cys Gly Asp Val Gly Thr Phe Gln Leu Ala Gly Lys
35 40 45

Gln Val Val Leu Leu Ser Gly Ser His Ala Asn Glu Phe Phe Phe Arg
50 55 60

Ala Gly Asp Asp Asp Leu Asp Gln Ala Lys Ala Tyr Pro Phe Met Thr
65 70 75 80

Pro Ile Phe Gly Glu Gly Val Val Phe Asp Ala Ser Pro Glu Arg Arg
85 90 95

Lys Glu Met Leu His Asn Ala Ala Leu Arg Gly Glu Gln Met Lys Gly
100 105 110

His Ala Ala Thr Ile Glu Asp Gln Val Arg Arg Met Ile Ala Asp Trp
115 120 125

Gly Glu Ala Gly Glu Ile Asp Leu Leu Asp Phe Phe Ala Glu Leu Thr
130 135 140

Ile Tyr Thr Ser Ser Ala Cys Leu Ile Gly Lys Lys Phe Arg Asp Gln
145 150 155 160

Leu Asp Gly Arg Phe Ala Lys Leu Tyr His Glu Leu Glu Arg Gly Thr
165 170 175

Asp Pro Leu Ala Tyr Val Asp Pro Tyr Leu Pro Ile Glu Ser Phe Arg
180 185 190

Arg Arg Asp Glu Ala Arg Asn Gly Leu Val Ala Leu Val Ala Asp Ile
195 200 205

Met Asn Gly Arg Ile Ala Asn Pro Pro Thr Asp Lys Ser Asp Arg Asp
210 215 220

Met Leu Asp Val Leu Ile Ala Val Lys Ala Glu Thr Gly Thr Pro Arg
225 230 235 240

Phe Ser Ala Asp Glu Ile Thr Gly Met Phe Ile Ser Met Met Phe Ala
 245 250 255
 Gly His His Thr Ser Ser Gly Thr Ala Ser Trp Thr Leu Ile Glu Leu
 260 265 270
 Met Arg His Arg Asp Ala Tyr Ala Ala Val Ile Asp Glu Leu Asp Glu
 275 280 285
 Leu Tyr Gly Asp Gly Arg Ser Val Ser Phe His Ala Leu Arg Gln Ile
 290 295 300
 Pro Gln Leu Glu Asn Val Leu Lys Glu Thr Leu Arg Leu His Pro Pro
 305 310 315 320
 Leu Ile Ile Leu Met Arg Val Ala Lys Gly Glu Phe Glu Val Gln Gly
 325 330 335
 His Arg Ile His Glu Gly Asp Leu Val Ala Ala Ser Pro Ala Ile Ser
 340 345 350
 Asn Arg Ile Pro Glu Asp Phe Pro Asp Pro His Asp Phe Val Pro Ala
 355 360 365
 Arg Tyr Glu Gln Pro Arg Gln Glu Asp Leu Leu Asn Arg Trp Thr Trp
 370 375 380
 Ile Pro Phe Gly Ala Gly Arg His Arg Cys Val Gly Ala Ala Phe Ala
 385 390 395 400
 Ile Met Gln Ile Lys Ala Ile Phe Ser Val Leu Leu Arg Glu Tyr Glu
 405 410 415
 Phe Glu Met Ala Gln Pro Pro Glu Ser Tyr Arg Asn Asp His Ser Lys
 420 425 430
 Met Val Val Gln Leu Ala Gln Pro Ala Cys Val Arg Tyr Arg Arg Arg
 435 440 445
 Thr Gly Val His His His His
 450 455

<210> 9
 <211> 504
 <212> PRT
 <213> Rat

<220>
 <223> CYP3A1

<400> 9

Met Asp Leu Leu Ser Ala Leu Thr Leu Glu Thr Trp Val Leu Leu Ala
 1 5 10 15
 Val Val Leu Val Leu Leu Tyr Gly Phe Gly Thr Arg Thr His Gly Leu
 20 25 30
 Phe Lys Lys Gln Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Phe Gly
 35 40 45

Thr Val Leu Asn Tyr Tyr Met Gly Leu Trp Lys Phe Asp Val Glu Cys
 50 55 60
 His Lys Lys Tyr Gly Lys Ile Trp Gly Leu Phe Asp Gly Gln Met Pro
 65 70 75 80
 Leu Phe Ala Ile Thr Asp Thr Glu Met Ile Lys Asn Val Leu Val Lys
 85 90 95
 Glu Cys Phe Ser Val Phe Thr Asn Arg Arg Asp Phe Gly Pro Val Gly
 100 105 110
 Ile Met Gly Lys Ala Val Ser Val Ala Lys Asp Glu Glu Trp Lys Arg
 115 120 125
 Tyr Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu
 130 135 140
 Met Phe Pro Ile Ile Glu Gln Tyr Gly Asp Ile Leu Val Lys Tyr Leu
 145 150 155 160
 Lys Gln Glu Ala Glu Thr Gly Lys Pro Val Thr Met Lys Lys Val Phe
 165 170 175
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn
 180 185 190
 Val Asp Ser Leu Asn Asn Pro Lys Asp Pro Phe Val Glu Lys Thr Lys
 195 200 205
 Lys Leu Leu Arg Phe Asp Phe Phe Asp Pro Leu Phe Leu Ser Val Val
 210 215 220
 Leu Phe Pro Phe Leu Thr Pro Ile Tyr Glu Met Leu Asn Ile Cys Met
 225 230 235 240
 Phe Pro Lys Asp Ser Ile Glu Phe Phe Lys Lys Phe Val Tyr Arg Met
 245 250 255
 Lys Glu Thr Arg Leu Asp Ser Val Gln Lys His Arg Val Asp Phe Leu
 260 265 270
 Gln Leu Met Met Asn Ala His Asn Asp Ser Lys Asp Lys Glu Ser His
 275 280 285
 Thr Ala Leu Ser Asp Met Glu Ile Thr Ala Gln Ser Ile Ile Phe Ile
 290 295 300
 Phe Ala Gly Tyr Glu Pro Thr Ser Ser Thr Leu Ser Phe Val Leu His
 305 310 315 320
 Ser Leu Ala Thr His Pro Asp Thr Gln Lys Lys Leu Gln Glu Glu Ile
 325 330 335
 Asp Arg Ala Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Met
 340 345 350
 Glu Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr
 355 360 365

Pro Ile Gly Asn Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile
370 375 380

Asn Gly Val Phe Met Pro Lys Gly Ser Val Val Met Ile Pro Ser Tyr
385 390 395 400

Ala Leu His Arg Asp Pro Gln His Trp Pro Glu Pro Glu Glu Phe Arg
405 410 415

Pro Glu Arg Phe Ser Lys Glu Asn Lys Gly Ser Ile Asp Pro Tyr Val
420 425 430

Tyr Leu Pro Phe Gly Asn Gly Pro Arg Asn Cys Ile Gly Met Arg Phe
435 440 445

Ala Leu Met Asn Met Lys Leu Ala Leu Thr Lys Val Leu Gln Asn Phe
450 455 460

Ser Phe Gln Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Arg
465 470 475 480

Gln Gly Leu Leu Gln Pro Thr Lys Pro Ile Ile Leu Lys Val Val Pro
485 490 495

Arg Asp Glu Ile Ile Thr Gly Ser
500

<210> 10

<211> 503

<212> PRT

<213> Homo sapiens

<220>

<223> CYP3A3

<400> 10

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val
1 5 10 15

Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe
20 25 30

Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn
35 40 45

Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His
50 55 60

Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val
65 70 75 80

Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Leu Val Leu Val Lys Glu
85 90 95

Cys Tyr Ser Val Phe Thr Asn Arg Glu Pro Phe Gly Pro Val Gly Phe
100 105 110

Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu

115					120					125					
Arg	Ser	Leu	Leu	Ser	Pro	Thr	Phe	Thr	Ser	Gly	Lys	Leu	Lys	Glu	Met
130						135					140				
Val	Pro	Ile	Ile	Ala	Gln	Tyr	Gly	Asp	Val	Leu	Val	Arg	Asn	Leu	Arg
145					150					155					160
Arg	Glu	Arg	Glu	Thr	Gly	Lys	Pro	Val	Thr	Leu	Lys	Asp	Val	Phe	Gly
				165					170					175	
Ala	Tyr	Ser	Met	Asp	Val	Ile	Thr	Ser	Ser	Ser	Phe	Gly	Val	Asn	Val
			180					185					190		
Asp	Ser	Leu	Asn	Asn	Pro	Gln	Asp	Pro	Leu	Val	Glu	Asn	Thr	Lys	Lys
		195					200					205			
Leu	Leu	Arg	Phe	Asp	Phe	Leu	Asp	Pro	Phe	Phe	Leu	Ser	Ile	Thr	Val
	210					215					220				
Phe	Pro	Phe	Leu	Ile	Pro	Ile	Leu	Glu	Val	Leu	Asn	Ile	Cys	Val	Phe
225					230					235					240
Pro	Arg	Glu	Val	Thr	Asn	Phe	Leu	Arg	Lys	Ala	Val	Lys	Arg	Met	Lys
				245					250					255	
Glu	Ser	Arg	Leu	Glu	Asp	Thr	Gln	Lys	His	Arg	Val	Asp	Phe	Leu	Gln
			260					265					270		
Leu	Met	Ile	Asp	Ser	His	Lys	Asn	Ser	Lys	Glu	Thr	Glu	Ser	His	Lys
		275					280					285			
Ala	Leu	Ser	Asp	Leu	Glu	Leu	Val	Ala	Gln	Ser	Ile	Ile	Phe	Ile	Phe
	290					295					300				
Ala	Gly	Tyr	Glu	Thr	Thr	Ser	Ser	Val	Leu	Ser	Phe	Ile	Met	Tyr	Glu
305					310					315					320
Leu	Ala	Thr	His	Pro	Asp	Val	Gln	Gln	Lys	Leu	Gln	Glu	Glu	Ile	Asp
				325					330					335	
Ala	Val	Leu	Pro	Asn	Lys	Ala	Pro	Pro	Thr	Tyr	Asp	Thr	Val	Leu	Gln
			340					345					350		
Met	Glu	Tyr	Leu	Asp	Met	Val	Val	Asn	Glu	Thr	Leu	Arg	Leu	Phe	Pro
		355					360					365			
Ile	Ala	Met	Arg	Leu	Glu	Arg	Val	Cys	Lys	Lys	Asp	Val	Glu	Ile	Asn
	370					375					380				
Gly	Met	Phe	Ile	Pro	Lys	Gly	Trp	Val	Val	Met	Ile	Pro	Ser	Tyr	Ala
385					390					395					400
Leu	His	Arg	Asp	Pro	Lys	Tyr	Trp	Thr	Glu	Pro	Glu	Lys	Phe	Leu	Pro
				405					410					415	
Glu	Arg	Phe	Ser	Lys	Lys	Asn	Lys	Asp	Asn	Ile	Asp	Pro	Tyr	Ile	Tyr
			420					425					430		
Thr	Pro	Phe	Gly	Ser	Gly	Pro	Arg	Asn	Cys	Ile	Gly	Met	Arg	Phe	Ala
			435				440					445			

Leu Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser
 450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu Gly
 465 470 475 480

Gly Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser Arg
 485 490 495

Asp Gly Thr Val Ser Gly Ala
 500

<210> 11
 <211> 502
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CYP3A4

<400> 11

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val
 1 5 10 15

Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe
 20 25 30

Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn
 35 40 45

Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His
 50 55 60

Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val
 65 70 75 80

Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu
 85 90 95

Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly Phe
 100 105 110

Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu
 115 120 125

Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met
 130 135 140

Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu Arg
 145 150 155 160

Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe Gly
 165 170 175

Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn Ile
 180 185 190

Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys Lys

195	200	205
Leu Leu Arg Phe Asp Phe Leu Asp Pro Phe Phe Leu Ser Ile Thr Val		
210	215	220
Phe Pro Phe Leu Ile Pro Ile Leu Glu Val Leu Asn Ile Cys Val Phe		
225	230	235 240
Pro Arg Glu Val Thr Asn Phe Leu Arg Lys Ser Val Lys Arg Met Lys		
	245	250 255
Glu Ser Arg Leu Glu Asp Thr Gln Lys His Arg Val Asp Phe Leu Gln		
	260	265 270
Leu Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Glu Ser His Lys Ala		
	275	280 285
Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe Ala		
	290	295 300
Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Met Tyr Glu Leu		
305	310	315 320
Ala Thr His Pro Val Asp Gln Gln Lys Leu Gln Glu Glu Ile Asp Ala		
	325	330 335
Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln Met		
	340	345 350
Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro Ile		
	355	360 365
Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn Gly		
	370	375 380
Met Phe Ile Pro Lys Gly Trp Val Val Met Ile Pro Ser Tyr Ala Leu		
385	390	395 400
His Arg Asp Pro Lys Tyr Met Thr Glu Pro Glu Lys Phe Leu Pro Glu		
	405	410 415
Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr Thr		
	420	425 430
Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala Leu		
	435	440 445
Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser Phe		
	450	455 460
Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu Gly Gly		
465	470	475 480
Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser Arg Asp		
	485	490 495
Gly Thr Val Ser Gly Ala		
	500	

<211> 502
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CYP3A5

<400> 12

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Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala
1          5          10          15

Val Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu
          20          25          30

Phe Lys Arg Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Leu Leu Gly
          35          40          45

Asn Val Leu Ser Tyr Arg Gln Gly Leu Trp Lys Phe Asp Thr Glu Cys
          50          55          60

Tyr Lys Lys Tyr Gly Lys Met Trp Gly Thr Tyr Glu Gly Gln Leu Pro
65          70          75          80

Val Leu Ala Ile Thr Asp Pro Asp Val Ile Arg Thr Val Leu Val Lys
          85          90          95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Leu Gly Pro Val Gly
          100          105          110

Phe Met Lys Ser Ala Ile Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg
          115          120          125

Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
          130          135          140

Met Phe Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
145          150          155          160

Arg Arg Glu Ala Glu Lys Gly Lys Pro Val Thr Leu Lys Asp Ile Phe
          165          170          175

Gly Ala Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn
          180          185          190

Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Ser Thr Lys
          195          200          205

Lys Phe Leu Lys Phe Gly Phe Leu Asp Pro Leu Phe Leu Ser Ile Ile
          210          215          220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Val Ser Leu
225          230          235          240

Phe Pro Lys Asp Thr Ile Asn Phe Leu Ser Lys Ser Val Asn Arg Met
          245          250          255

Lys Lys Ser Arg Leu Asn Asp Lys Gln Lys His Arg Leu Asp Phe Leu
          260          265          270

Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Glu Ser His Lys

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275					280					285					
Ala	Leu	Ser	Asp	Leu	Glu	Leu	Ala	Ala	Gln	Ser	Ile	Ile	Phe	Ile	Phe
290						295					300				
Ala	Gly	Tyr	Glu	Thr	Thr	Ser	Ser	Val	Leu	Ser	Phe	Thr	Leu	Tyr	Glu
305					310					315					320
Leu	Ala	Thr	His	Pro	Asp	Val	Gln	Gln	Lys	Leu	Gln	Lys	Glu	Ile	Asp
				325					330					335	
Ala	Val	Leu	Pro	Asn	Lys	Ala	Pro	Pro	Thr	Tyr	Asp	Ala	Val	Val	Gln
			340					345					350		
Met	Glu	Tyr	Leu	Asp	Met	Val	Val	Asn	Glu	Thr	Leu	Arg	Leu	Phe	Pro
		355					360					365			
Val	Ala	Ile	Arg	Leu	Glu	Arg	Thr	Cys	Lys	Lys	Asp	Val	Glu	Ile	Asn
	370					375					380				
Gly	Val	Phe	Ile	Pro	Lys	Gly	Ser	Met	Val	Val	Ile	Pro	Thr	Tyr	Ala
385						390					395				400
Leu	His	His	Asp	Pro	Lys	Tyr	Trp	Thr	Glu	Pro	Glu	Glu	Phe	Arg	Pro
			405						410					415	
Glu	Arg	Phe	Ser	Lys	Lys	Lys	Asp	Ser	Ile	Asp	Pro	Tyr	Ile	Tyr	Thr
			420					425					430		
Pro	Phe	Gly	Thr	Gly	Pro	Arg	Asn	Cys	Ile	Gly	Met	Arg	Phe	Ala	Leu
		435					440					445			
Met	Asn	Met	Lys	Leu	Ala	Leu	Ile	Arg	Val	Leu	Gln	Asn	Phe	Ser	Phe
	450					455					460				
Lys	Pro	Cys	Lys	Glu	Thr	Gln	Ile	Pro	Leu	Lys	Leu	Asp	Thr	Gln	Gly
465					470					475					480
Leu	Leu	Gln	Pro	Glu	Lys	Pro	Ile	Val	Leu	Lys	Val	Asp	Ser	Arg	Asp
			485						490					495	
Gly	Thr	Leu	Ser	Gly	Glu										
			500												

<210> 13

<211> 503

<212> PRT

<213> Homo sapiens

<220>

<223> CYP3A43

<400> 13

Met	Asp	Leu	Ile	Pro	Asn	Phe	Ala	Met	Glu	Thr	Trp	Val	Leu	Val	Ala
1				5					10					15	

Thr	Ser	Leu	Val	Leu	Leu	Tyr	Ile	Tyr	Gly	Thr	His	Ser	His	Lys	Leu
			20					25					30		

Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly
 35 40 45
 Thr Ile Leu Phe Tyr Leu Arg Gly Leu Trp Asn Phe Asp Arg Glu Cys
 50 55 60
 Asn Glu Lys Tyr Gly Glu Met Trp Gly Leu Tyr Glu Gly Gln Gln Pro
 65 70 75 80
 Met Leu Val Ile Met Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
 85 90 95
 Glu Cys Tyr Ser Val Phe Thr Asn Gln Met Pro Leu Gly Pro Met Gly
 100 105 110
 Phe Leu Lys Ser Ala Leu Ser Phe Ala Glu Asp Glu Glu Trp Lys Arg
 115 120 125
 Ile Arg Thr Leu Leu Ser Pro Ala Phe Thr Ser Val Lys Phe Lys Glu
 130 135 140
 Met Val Pro Ile Ile Ser Gln Cys Gly Asp Met Leu Val Arg Ser Leu
 145 150 155 160
 Arg Gln Glu Ala Glu Asn Ser Lys Ser Ile Asn Leu Lys Asp Phe Phe
 165 170 175
 Gly Ala Tyr Thr Met Asp Val Ile Thr Gly Thr Leu Phe Gly Val Asn
 180 185 190
 Leu Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Leu Lys Asn Met Lys
 195 200 205
 Lys Leu Leu Lys Leu Asp Phe Leu Asp Pro Phe Leu Leu Leu Ile Ser
 210 215 220
 Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Ile Gly Leu
 225 230 235 240
 Phe Pro Lys Asp Val Thr His Phe Leu Lys Asn Ser Ile Glu Arg Met
 245 250 255
 Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Phe
 260 265 270
 Gln Gln Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Lys Ser His Lys
 275 280 285
 Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Ile Ile Phe
 290 295 300
 Ala Ala Tyr Asp Thr Thr Ser Thr Thr Leu Pro Phe Ile Met Tyr Glu
 305 310 315 320
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp
 325 330 335
 Ala Val Leu Pro Asn Lys Ala Pro Val Thr Tyr Asp Ala Leu Val Gln
 340 345 350
 Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro

355 360 365
 Val Val Ser Arg Val Thr Arg Val Cys Lys Lys Asp Ile Glu Ile Asn
 370 375 380
 Gly Val Phe Ile Pro Lys Gly Leu Ala Val Met Val Pro Ile Tyr Ala
 385 390 395 400
 Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Cys Pro
 405 410 415
 Glu Arg Phe Ser Lys Lys Asn Lys Asp Ser Ile Asp Leu Tyr Arg Tyr
 420 425 430
 Ile Pro Phe Gly Ala Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
 435 440 445
 Leu Thr Asn Ile Lys Leu Ala Val Ile Arg Ala Leu Gln Asn Phe Ser
 450 455 460
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asp Asn Leu
 465 470 475 480
 Pro Ile Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val His Leu Arg
 485 490 495
 Asp Gly Ile Thr Ser Gly Pro
 500

<210> 14
 <211> 501
 <212> PRT
 <213> Rabbit

<220>
 <223> CYP3A6

<400> 14

Met Asp Leu Ile Phe Ser Leu Glu Thr Trp Val Leu Leu Ala Ala Ser
 1 5 10 15
 Leu Val Leu Leu Tyr Leu Tyr Gly Thr Ser Thr His Gly Leu Phe Lys
 20 25 30
 Lys Met Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Ile Gly Thr Ile
 35 40 45
 Leu Glu Tyr Arg Lys Gly Ile Trp Asp Phe Asp Ile Glu Cys Arg Lys
 50 55 60
 Lys Tyr Gly Lys Met Trp Gly Leu Phe Asp Gly Arg Gln Pro Leu Met
 65 70 75 80
 Val Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu Cys
 85 90 95
 Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Val Gly Phe Met
 100 105 110

Lys Lys Ala Val Ser Ile Ser Glu Asp Glu Asp Trp Lys Arg Val Arg
 115 120 125
 Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met Leu
 130 135 140
 Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Lys Asn Leu Arg Gln
 145 150 155 160
 Glu Ala Glu Lys Gly Lys Pro Val Asp Leu Lys Glu Ile Phe Gly Ala
 165 170 175
 Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn Ile Asp
 180 185 190
 Ser Leu Arg Asn Pro Gln Asp Pro Phe Val Lys Asn Val Arg Arg Leu
 195 200 205
 Leu Lys Phe Ser Phe Phe Asp Pro Leu Leu Leu Ser Ile Thr Leu Phe
 210 215 220
 Pro Phe Leu Thr Pro Ile Phe Glu Ala Leu His Ile Ser Met Phe Pro
 225 230 235 240
 Lys Asp Val Met Asp Phe Leu Lys Thr Ser Val Glu Lys Ile Lys Asp
 245 250 255
 Asp Arg Leu Lys Asp Lys Gln Lys Arg Arg Val Asp Phe Leu Gln Leu
 260 265 270
 Met Ile Asn Ser Gln Asn Ser Lys Glu Ile Asp Ser His Lys Ala Leu
 275 280 285
 Asp Asp Ile Glu Val Val Ala Gln Ser Ile Ile Ile Leu Phe Ala Gly
 290 295 300
 Tyr Glu Thr Thr Ser Ser Thr Leu Ser Phe Ile Met His Leu Leu Ala
 305 310 315 320
 Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp Thr Leu
 325 330 335
 Leu Pro Asn Lys Glu Leu Ala Thr Tyr Asp Thr Leu Val Lys Met Glu
 340 345 350
 Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro Ile Ala
 355 360 365
 Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Asp Ile Asn Gly Thr
 370 375 380
 Phe Ile Pro Lys Gly Thr Ile Val Met Met Pro Thr Tyr Ala Leu His
 385 390 395 400
 Arg Asp Pro Gln His Trp Thr Glu Pro Asp Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Ser Lys Lys Asn Lys Asp Asn Ile Asn Pro Tyr Ile Tyr His Pro
 420 425 430
 Phe Gly Ala Gly Pro Arg Asn Cys Leu Gly Met Arg Phe Ala Leu Met

435 440 445
 Asn Ile Lys Leu Ala Leu Val Arg Leu Met Gln Asn Phe Ser Phe Lys
 450 455 460
 Leu Cys Lys Glu Thr Gln Val Pro Leu Lys Leu Gly Lys Gln Gly Leu
 465 470 475 480
 Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val Val Ser Arg Asp Gly
 485 490 495
 Ile Ile Arg Gly Ala
 500

 <210> 15
 <211> 503
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> CYP3A7

 <400> 15
 Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala
 1 5 10 15
 Val Ser Leu Ile Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu
 20 25 30
 Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly
 35 40 45
 Asn Ala Leu Ser Phe Arg Lys Gly Tyr Trp Thr Phe Asp Met Glu Cys
 50 55 60
 Tyr Lys Lys Tyr Arg Lys Val Trp Gly Ile Tyr Asp Cys Gln Gln Pro
 65 70 75 80
 Met Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
 85 90 95
 Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly
 100 105 110
 Phe Met Lys Asn Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg
 115 120 125
 Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
 130 135 140
 Met Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
 145 150 155 160
 Arg Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys His Val Phe
 165 170 175
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Ser
 180 185 190

Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys
 195 200 205
 Lys Leu Leu Arg Phe Asn Pro Leu Asp Pro Phe Val Leu Ser Ile Lys
 210 215 220
 Val Phe Pro Phe Leu Thr Pro Ile Leu Glu Ala Leu Asn Ile Thr Val
 225 230 235 240
 Phe Pro Arg Lys Val Ile Ser Phe Leu Thr Lys Ser Val Lys Gln Ile
 245 250 255
 Lys Glu Gly Arg Leu Lys Glu Thr Gln Lys His Arg Val Asp Phe Leu
 260 265 270
 Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Asp Ser Glu Thr His Lys
 275 280 285
 Ala Leu Ser Asp Leu Glu Leu Met Ala Gln Ser Ile Ile Phe Ile Phe
 290 295 300
 Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Ile Tyr Glu
 305 310 315 320
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Val Gln Lys Glu Ile Asp
 325 330 335
 Thr Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln
 340 345 350
 Leu Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro
 355 360 365
 Val Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn
 370 375 380
 Gly Met Phe Ile Pro Lys Gly Val Val Val Met Ile Pro Ser Tyr Val
 385 390 395 400
 Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu Pro
 405 410 415
 Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr
 420 425 430
 Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
 435 440 445
 Leu Val Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
 450 455 460
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Arg Phe Gly
 465 470 475 480
 Gly Leu Leu Leu Thr Glu Lys Pro Ile Val Leu Lys Ala Glu Ser Arg
 485 490 495
 Asp Glu Thr Val Ser Gly Ala
 500

<210> 16
 <211> 503
 <212> PRT
 <213> Dog

<220>
 <223> CYP3A12

<400> 16

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Met Asp Leu Ile Pro Ser Phe Ser Thr Glu Thr Trp Leu Leu Leu Ala
1          5          10          15

Ile Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Thr His Gly Ile
20          25          30

Phe Arg Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Val Gly
35          40          45

Thr Ala Leu Gly Tyr Arg Asn Gly Phe Tyr Val Phe Asp Met Lys Cys
50          55          60

Phe Ser Lys Tyr Gly Arg Met Trp Gly Phe Tyr Asp Gly Arg Gln Pro
65          70          75          80

Val Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
85          90          95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Thr Leu Gly Pro Val Gly
100         105         110

Phe Met Lys Ser Ala Ile Ser Leu Ser Glu Asp Glu Glu Trp Lys Arg
115         120         125

Met Arg Thr Leu Leu Ser Pro Thr Phe Thr Thr Gly Lys Leu Lys Glu
130         135         140

Met Phe Pro Ile Ile Gly Gln Tyr Gly Asp Val Leu Val Asn Asn Leu
145         150         155         160

Arg Lys Glu Ala Glu Lys Gly Lys Ala Ile Asn Leu Lys Asp Val Phe
165         170         175

Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn
180         185         190

Ile Asp Ser Leu Asn His Pro Gln Asp Pro Phe Val Glu Asn Thr Lys
195         200         205

Lys Leu Leu Lys Phe Asp Phe Leu Asp Pro Phe Phe Phe Ser Ile Leu
210         215         220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ile Leu Asn Ile Trp Leu
225         230         235         240

Phe Pro Lys Lys Val Thr Asp Phe Phe Arg Lys Ser Val Glu Arg Met
245         250         255

Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Leu
260         265         270

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Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Thr His Lys
 275 280 285
 Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe
 290 295 300
 Ala Gly Tyr Glu Thr Thr Ser Thr Ser Leu Ser Phe Leu Met Tyr Glu
 305 310 315 320
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp
 325 330 335
 Ala Thr Phe Pro Asn Lys Ala Leu Pro Thr Tyr Asp Ala Leu Val Gln
 340 345 350
 Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr Pro
 355 360 365
 Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Ser
 370 375 380
 Gly Val Phe Ile Pro Lys Gly Thr Val Val Met Val Pro Thr Phe Thr
 385 390 395 400
 Leu His Arg Asp Gln Ser Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro
 405 410 415
 Glu Arg Phe Ser Arg Lys Asn Lys Asp Ser Ile Asn Pro Tyr Thr Tyr
 420 425 430
 Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
 435 440 445
 Ile Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
 450 455 460
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asn Ala Gln
 465 470 475 480
 Gly Ile Ile Gln Pro Glu Lys Pro Ile Val Leu Lys Val Glu Pro Arg
 485 490 495
 Asp Gly Ser Val Asn Gly Ala
 500

<210> 17

<211> 503

<212> PRT

<213> Pig

<220>

<223> CYP3A29

<400> 17

Met Asp Leu Ile Pro Gly Phe Ser Thr Glu Thr Trp Val Leu Leu Ala
 1 5 10 15
 Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Ser His Gly Leu
 20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Arg Pro Leu Pro Tyr Phe Gly
 35 40 45
 Asn Ile Leu Gly Tyr Arg Lys Gly Val Asp His Phe Asp Lys Lys Cys
 50 55 60
 Phe Gln Gln Tyr Gly Lys Met Trp Gly Val Tyr Asp Gly Arg Gln Pro
 65 70 75 80
 Leu Leu Ala Val Thr Asp Pro Asn Met Ile Lys Ser Val Leu Val Lys
 85 90 95
 Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Leu Gly
 100 105 110
 Ala Met Arg Asn Ala Leu Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg
 115 120 125
 Ile Arg Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
 130 135 140
 Met Phe Pro Ile Ile Ser His Tyr Gly Asp Leu Leu Val Ser Asn Leu
 145 150 155 160
 Arg Lys Glu Ala Glu Lys Gly Lys Pro Val Thr Met Lys Asp Ile Phe
 165 170 175
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ala Phe Gly Val Asn
 180 185 190
 Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Ser Lys
 195 200 205
 Lys Leu Leu Lys Phe Ser Phe Phe Asp Pro Phe Leu Leu Ser Leu Ile
 210 215 220
 Phe Phe Pro Phe Leu Thr Pro Ile Phe Glu Val Leu Asn Ile Thr Leu
 225 230 235 240
 Phe Pro Lys Ser Ser Val Asn Phe Phe Thr Lys Ser Val Lys Arg Met
 245 250 255
 Lys Glu Ser Arg Leu Thr Asp Gln Gln Lys Arg Arg Val Asp Leu Leu
 260 265 270
 Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Pro His Lys
 275 280 285
 Ser Leu Ser Asn Glu Glu Leu Val Ala Gln Gly Ile Ile Phe Ile Phe
 290 295 300
 Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Leu Leu Ala Tyr Glu
 305 310 315 320
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Glu
 325 330 335
 Ala Thr Phe Pro Asn Lys Ala Pro Pro Thr Tyr Asp Ala Leu Ala Gln
 340 345 350

Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro
 355 360 365

Ile Ala Ala Arg Leu Glu Arg Ala Cys Lys Lys Asp Val Glu Ile His
 370 375 380

Gly Val Phe Val Pro Lys Gly Thr Val Val Val Val Pro Val Phe Val
 385 390 395 400

Leu His Arg Asp Pro Asp Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro
 405 410 415

Glu Arg Phe Ser Lys Lys His Lys Asp Thr Ile Asn Pro Tyr Thr Tyr
 420 425 430

Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
 435 440 445

Leu Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
 450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Thr Thr Gln
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Gly Leu Thr Gln Pro Glu Lys Pro Val Val Leu Lys Ile Leu Pro Arg
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Asp Gly Thr Val Ser Gly Ala
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<400> 18

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Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Ile
 20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Leu Gly
 35 40 45

Thr Ile Leu Ala Tyr Gln Lys Gly Phe Trp Glu Cys Asp Ile Gln Cys
 50 55 60

His Lys Lys Tyr Gly Lys Met Trp Gly Leu Tyr Asp Gly Arg Gln Pro
 65 70 75 80

Val Leu Ala Ile Thr Asp Pro Asp Ile Ile Lys Thr Val Leu Val Lys
 85 90 95

Glu Cys Tyr Ser Thr Phe Thr Asn Arg Arg Arg Phe Gly Pro Val Gly
 100 105 110
 Ile Leu Lys Lys Ala Ile Ser Ile Ser Glu Asn Glu Glu Trp Lys Arg
 115 120 125
 Ile Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu
 130 135 140
 Met Phe Pro Ile Ile Asn Gln Phe Thr Asp Val Leu Val Arg Asn Met
 145 150 155 160
 Arg Gln Gly Leu Gly Glu Gly Lys Pro Thr Ser Met Lys Asp Ile Phe
 165 170 175
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ala Thr Ser Phe Gly Val Asn
 180 185 190
 Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Lys Ile Lys
 195 200 205
 Lys Leu Leu Lys Phe Asp Ile Phe Asp Pro Leu Phe Leu Ser Val Thr
 210 215 220
 Leu Phe Pro Phe Leu Thr Pro Val Phe Asp Ala Leu Asn Val Ser Leu
 225 230 235 240
 Phe Pro Arg Asp Val Ile Ser Phe Phe Thr Thr Ser Val Glu Arg Met
 245 250 255
 Lys Glu Asn Arg Met Lys Glu Lys Glu Lys Gln Arg Val Asp Phe Leu
 260 265 270
 Gln Leu Met Ile Asn Ser Gln Asn Tyr Lys Thr Lys Glu Ser His Lys
 275 280 285
 Ala Leu Ser Asp Val Glu Ile Val Ala Gln Ser Val Ile Phe Ile Phe
 290 295 300
 Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Phe Ala Leu Tyr Leu
 305 310 315 320
 Leu Ala Ile His Pro Asp Val Gln Lys Lys Leu Gln Asp Glu Ile Asp
 325 330 335
 Ala Ala Leu Pro Asn Lys Ala Pro Ala Thr Tyr Asp Thr Leu Leu Gln
 340 345 350
 Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro
 355 360 365
 Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Thr Asp Val Glu Ile Asn
 370 375 380
 Gly Leu Phe Ile Pro Lys Gly Thr Val Val Met Ile Pro Thr Phe Ala
 385 390 395 400
 Leu His Lys Asp Pro Lys Tyr Trp Pro Glu Pro Glu Glu Phe Arg Pro
 405 410 415

Glu Arg Phe Ser Lys Lys Asn Gln Asp Ser Ile Asn Pro Tyr Met Tyr
420 425 430

Leu Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Leu Ile Asn Met Lys Val Ala Leu Val Arg Val Leu Gln Asn Phe Thr
450 455 460

Val Gln Pro Cys Lys Glu Thr Glu Ile Pro Leu Lys Leu Ser Lys Gln
465 470 475 480

Gly Leu Leu Gln Pro Glu Asn Pro Leu Leu Leu Lys Val Val Ser Arg
485 490 495

Asp Glu Thr Val Ser Asp Glu
500